

Appendix A

BLASTP 2.0.8 [Jan-05-1999]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= rlr72.pk0015.b2.fis1 3/15/99 no filter, Becky
(410 letters)

Database: /blast/data/2.0/2/nr
361,503 sequences; 110,384,461 total letters

Searching.....done

Sequences producing significant alignments:	Score (bits)	E Value	pLog
gi 3165581 (AF067942) similar to lysosomal acid lipases (SW:P385...	212	5e-54	53.30
gi 3877594 emb CAB01973 (Z79696) predicted using Genefinder; Si...	211	6e-54	53.22
gi 1083069 pir JC4017 triacylglycerol lipase (EC 3.1.1.3) PGE p...	211	8e-54	53.10
gi 126306 sp P07098 LIPG_HUMAN TRIACYLGLYCEROL LIPASE PRECURSOR ...	207	1e-52	52.00
gi 758064 emb CAA29414 (X05997) gastric lipase precursor [Homo ...	207	1e-52	
gi 126307 sp P04634 LIPG_RAT TRIACYLGLYCEROL LIPASE PRECURSOR (L...	204	8e-52	
gi 2384863 (AF022976) Similar to lipase; R11G11.14 [Caenorhabdit...	199	4e-50	
gi 3041702 sp P80035 LIPG_CANFA TRIACYLGLYCEROL LIPASE PRECURSOR...	198	5e-50	
gi 505053 (U08464) lysosomal acid lipase [Homo sapiens] >gi 5064...	195	5e-49	
gi 585405 sp P38571 LIPA_HUMAN LYSOSOMAL ACID LIPASE/CHOLESTERYL...	195	5e-49	

>gi|3165581 (AF067942) similar to lysosomal acid lipases (SW:P38571)
[Caenorhabditis elegans]
Length = 403

Score = 212 bits (533), Expect = 5e-54
Identities = 122/370 (32%), Positives = 185/370 (49%), Gaps = 15/370 (4%)

Query: 49 QLLLPLGYPCTEHNVETKDGFLLSLQHHPHGKNAADSTG--PPVFLQHGLFQGGDTWFI 106
Q++ GYP + V T DG++L + IP GK G P VF+QHGL W +
Sbjct: 31 QIIRWGYPAMIYTVATDDGYILEMHRIPFGKTNVTWPNKRPVVMQHGLLCASSDWVV 90

Query: 107 NSAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFDWDSWQELAEYDLLAMLG 166
N +QS G++ AD GFDVW+GN+RG +S H FWDWSW E+A YDL AM+
Sbjct: 91 NLPDQSAGFLFADAGFDVWLGNMGRGNTYSMKHKDLKPSHSFAFDWSWDEMATYDLNAMIN 150

Query: 167 YVYTVT-QSKILYVGHSQGTIMGLAALTMPE--IVKMISSAALLCPISYLDHVS--SFV 221
+V VT Q + Y+GHSQGT+ + L+ + K I L PI + H+ SF
Sbjct: 151 HVLEVTVGQDSVYYMGHSQGTITMFSHLSKDDGSFAKKIKKFFALAPIGSVKHIKGFSLFF 210

Query: 222 LRAVAMHLDQMLVTMGIHQNLFRSDMGVQIVDSLDCGEHVD---CNNLLSAITG-ENCCF 277
++ D G + + +C G V+ C+N+L I G E+ +
Sbjct: 211 ANYFSLEFDGWFDFGAGEFLPNNWAMKLAADKICGGLKVEADLCDNVFLIAGPESDQW 270

Query: 278 NTSRIDYYLEYEPHPSSTKNLHHLFQMIRKGTFAKYDYGLGNLRRYGHRLPPAFDLSSI 337
N +R+ Y ++P +ST+N+ H QM+ G YD+G N ++YG PP +D ++I
Sbjct: 271 NQTRVPVYATHDPAGTSTQNIVHWMQMVHGGVPAYDWGKTNTKKKYQANPPEYDFTAI 330

Query: 338 PESLPIWMGYGGLDALADVDVQ---RTIRELGSTPELLYIGDYGHIDFVMSVKAKDDVY 394
+ I++ + D LAD DV T + ++ DY H+DF ++A DD+Y
Sbjct: 331 -KGTKIYLYWSDADWLADTPDVPDYLLTRLNPAIVAQNHLDPYNHLDFTWGLRAPDDIY 389

Query: 395 VDLIRFLREN 404
I+ ++
Sbjct: 390 RPAIKLCTDD 399

>gi|3877594|emb|CAB01973| (Z79696) predicted using Genefinder; Similarity to Rat lipase
(SW:LIPG_RAT); cDNA EST yk310f9.3 comes from this gene;

cdNA EST yk387d12.3 comes from this gene; cdNA EST
yk300a8.3 comes from this gene; cdNA EST yk310f9.5 comes
f...
Length = 405

Score = 211 bits (532), Expect = 6e-54
Identities = 119/370 (32%), Positives = 193/370 (52%), Gaps = 16/370 (4%)

Query: 49 QLLLPLGYPCTEHNVETKDGFLLSLQHIPHGKNAADSTG--PPVFLQHGLFQGGDTWFI 106
Q+++ GYP ++V T+DG++L L IP+GK G P VF+QHGL W +
Sbjct: 33 QIIMRWGYPAMIYDVTEDGYILELHRIPIYGKTNVTPNGKKPVVFMQHGLECSSSNWVV 92

Query: 107 NSAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFDWDSWQELAEYDLLAMLG 166
N +S ++ AD G+DVW+GN RG +S H FWDWSW E+ +YDL AM+
Sbjct: 93 NLPTESA AFLFADAGYDVWLG NFRGNTYSMKHKNLKPSHSAFWDWSWDEMQQYDLPAMIE 152

Query: 167 VYVTVT-QSKILYVGHSQGTIMGLAALTMPEI--VKMISSAALLCPISYLDHVSAS--FV 221
VT Q + Y+GHSQGT+ + L+ ++ I L P+ + H+ + F
Sbjct: 153 KALEVTGQDSLYYIGHSQGTITMFSRLSEDKVWGWNKIKKFFALAPVGSVKHIKALKFF 212

Query: 222 LRAVAMHLDQMLVTMGIHQNLNFRSDMGVQIVDSLCDGEHVD---CNNLLSAITG-ENCCF 277
++ D G + + + +S+C G V+ C++++ I G E+
Sbjct: 213 ADYFSLFDGWFDFVGSGEFLPNNWIMKLVSSEVACGLKVEAGVCDVDFLIAGPESNQL 272

Query: 278 NTSRIDYYLEYEPHPSSTKNLHHLFQMIRKGTFAKYDGLGNLRRYGHRLPPAFDLSSI 337
N +R+ Y+ + P +ST+N+ H QM+R G KYDYG GN + YG PA+D +++
Sbjct: 273 NATRVPIYVAHTPAGTSTQNIWHVIQMRHGGTPKYDYGEGKNKKHYQANVPAYDFTTV 332

Query: 338 PESLPIWMGYGGLDALA---DVTDVQRTIRELGSTPELLYIGDYGHIDFVMSVKAKDDVY 394
+ P+++ +G D LA DVT D T + + + DY H+DF+ ++A D+Y
Sbjct: 333 --NRPVLYWGDSDWLADPTDVTDFLLTHLNPSTVVQNNKLIDYNHLDFIWGLRAPKDIY 390

Query: 395 VDLIRFLREN 404
+I +R +
Sbjct: 391 EPIIDIVRND 400

>gi|1083069|pir||JC4017 triacylglycerol lipase (EC 3.1.1.3) PGE precursor - bovine
>gi|600757 (L26319) pregastric esterase [Bos taurus]
Length = 397

Score = 211 bits (531), Expect = 8e-54
Identities = 126/366 (34%), Positives = 193/366 (52%), Gaps = 16/366 (4%)

Query: 49 QLLLPLGYPCTEHNVETKDGFLLSLQHIPHGKNAAD-STGPPVFLQHGLFQGGDTWFIN 107
Q++ GYP H V T DG++L + IPHGKN A P VFLQHGL W N
Sbjct: 36 QMISYWGYPSEMHKVITADGYILQVYRIPHGKNANHLGQRPVVFLQHGLLG SATNWISN 95

Query: 108 SAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFDWDSWQELAEYDLLAMLGY 167
+ SLG++LAD G+DVW+GN RG W++ H +S FW +S+ E+AEYDL + + +
Sbjct: 96 LPKNSLGLLADAGYDVWLGNSRGNTWAQEHLYSPDSPEFWAFSFDMAEYDLPSTIDF 155

Query: 168 VYTVT-QSKILYVGHSQGTIMGLAAL-TMPEIVKMISSAALLCPISYLDHVSASFVLRV 225
+ T Q K+ YVGHSQGT +G A T P + + I L P++ + + + F A+
Sbjct: 156 ILRRTGQKKLHYVGHSQGTITIGFIAFSTSPTLAEIKVFIYALAPVATVKYTKSLFNKLAL 215

Query: 226 AMHLDQMLV---TMGIHQNLNFRSDMGVQIVDSLCDGEHVD---CNNLLSAITG-ENCCFNT 279
H ++ M +GV+ +C E +D C N L AITG +N FN
Sbjct: 216 IPHFLFKIIFGDKMFYPHTFLEQFLGVE---MCSRETLDVLCCKNALFAITGVNDKNFNM 271

Query: 280 SRIDYYLEYEPHPSSTKNLHHLFQMIRKGTFAKYDYL-LGNLRRYGHRLPPAFDLSSIP 338
SR+D Y+ + P +S +N H Q ++ G F +D+G NL Y PP ++L+++
Sbjct: 272 SRLDVYIAHNPAGTSVQNTLHWRQAVKSGKQAFDWGAPYQNLMHYHQPTPIYNLTAMN 331

Query: 339 ESLPIWMGYGGLDALADVTDVQRTIRELGSTPELLYIGDYGHIDFVMSVKAKDDVYVDLI 398
+ +W D LAD DV + +L + I +Y H+DF+ ++ A +VY +++
Sbjct: 332 VPIAWSADN--DLLADPQDVDFLLSKLSNLIYHKEIPNYNHLDFIWAMDAPQEVYNEIV 389

Query: 399 RFLREN 404
+ E+
Sbjct: 390 SLMAED 395

>gi|126306|sp|P07098|LIPG_HUMAN TRIACYLGLYCEROL LIPASE PRECURSOR (LIPASE, GASTRIC)
>gi|106904|pir||S07145 triacylglycerol lipase (EC
3.1.1.3) precursor, gastric - human
>gi|758063|emb|CAA29413| (X05997) gastric lipase
precursor [Homo sapiens]
Length = 398

Score = 207 bits (521), Expect = 1e-52

Identities = 129/369 (34%), Positives = 203/369 (54%), Gaps = 22/369 (5%)

Query: 49 QLLLPLGYPCTEHNVEKDGFLSLQHIPHGKNAADSTG--PPVFLQHGLFQGGDTWFI 106
Q++ GYP E+ V T+DG++L + IP+GK K + +TG P VFLQHGL W
Sbjct: 37 QMITYWGYPNEEYEVVTEGDGYILEVNRIPYGK-KNSGNTGQRPVVFLQHGLLASATNWIS 95

Query: 107 NSAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFDWDSWQELAEYDLLAMLG 166
N SL +ILAD G+DVW+GN RG W++ + +S FW +S+ E+A+YDL A +
Sbjct: 96 NLPNNSLAFILADAGYDVWLGNSRGNTWARRNLYSPDSVEFWAFSFDMAKYDLPATID 155

Query: 167 YVYTVT-QSKILYVGHSQGTIMGLAAL-TMPEIVKMISSAALLCPISYLDHVSASF-VLR 223
++ T Q ++ YVGHSQGT +G A T P + K I + L P++ + + + LR
Sbjct: 156 FIVKKTGQKQLHYVGHSQGTITIGFIAFSTNPSLAKRIKTFYALAPVATVKYTKSLINKLR 215

Query: 224 AVAMHLDQMLVTMGI-HQLNFRSDMGVQIVDSLCDGEHVD--CNNLLSAITG-ENCCFNT 279
V L + + I + NF + +C E ++ C+N L I G ++ FNT
Sbjct: 216 FVPQSLFKFIFGDKIFYPHNFFDQF---LATEVCSREMLNLLCSNALFIICGFDSKNFNT 272

Query: 280 SRIDYYLEYEPHPSSTKNLHHLFQMIRKGTFAKYDYGL-LGNLRRYGHRLPPAFDLSSIP 338
SR+D YL + P +S +N+ H Q ++ G F YD+G + N Y +PP +++++
Sbjct: 273 SRLDVYLSHNPAGTSVQNMFWHTQAVKSGKFQAYDWGSPVQNRMHYDQSQPPYYNVTAMN 332

Query: 339 ESLPIWMGYGGLDALADVTDVQRTIRELGSTPELly---IGDYGHIDFVMSVKAKDDVYV 395
+ +W GG D LAD DV + +L P L+Y I Y H+DF+ ++ A +VY
Sbjct: 333 VPIAVW--NGGKDLLADPQDVGLLLPKL---PNLIYHKEIPFYNHLDIFIWAMDAPQEVYN 387

Query: 396 DLIRFLREN 404
D++ + E+
Sbjct: 388 DIVSMISED 396

>gi|758064|emb|CAA29414| (X05997) gastric lipase precursor [Homo sapiens]
Length = 392

Score = 207 bits (521), Expect = 1e-52

Identities = 129/369 (34%), Positives = 203/369 (54%), Gaps = 22/369 (5%)

Query: 49 QLLLPLGYPCTEHNVEKDGFLSLQHIPHGKNAADSTG--PPVFLQHGLFQGGDTWFI 106
Q++ GYP E+ V T+DG++L + IP+GK K + +TG P VFLQHGL W
Sbjct: 31 QMITYWGYPNEEYEVVTEGDGYILEVNRIPYGK-KNSGNTGQRPVVFLQHGLLASATNWIS 89

Query: 107 NSAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFDWDSWQELAEYDLLAMLG 166
N SL +ILAD G+DVW+GN RG W++ + +S FW +S+ E+A+YDL A +
Sbjct: 90 NLPNNSLAFILADAGYDVWLGNSRGNTWARRNLYSPDSVEFWAFSFDMAKYDLPATID 149

Query: 167 YVYTVT-QSKILYVGHSQGTIMGLAAL-TMPEIVKMISSAALLCPISYLDHVSASF-VLR 223
++ T Q ++ YVGHSQGT +G A T P + K I + L P++ + + + LR
Sbjct: 150 FIVKKTGQKQLHYVGHSQGTITIGFIAFSTNPSLAKRIKTFYALAPVATVKYTKSLINKLR 209

Query: 224 AVAMHLDQMLVTMGI-HQLNFRSDMGVQIVDSLCDGEHVD--CNNLLSAITG-ENCCFNT 279
V L + + I + NF + +C E ++ C+N L I G ++ FNT
Sbjct: 210 FVPQSLFKFIFGDKIFYPHNFFDQF---LATEVCSREMLNLLCSNALFIICGFDSKNFNT 266

Query: 280 SRIDYYLEYEPHPSSTKNLHHLFQMIRKGTFAKYDYGL-LGNLRRYGHRLPPAFDLSSIP 338
SR+D YL + P +S +N+ H Q ++ G F YD+G + N Y +PP +++++
Sbjct: 267 SRLDVYLSHNPAGTSVQNMFWHTQAVKSGKFQAYDWGSPVQNRMHYDQSQPPYYNVTAMN 326

Query: 339 ESLPIWMGYGGLDALADVTDVQRTIRELGSTPELly---IGDYGHIDFVMSVKAKDDVYV 395
+ +W GG D LAD DV + +L P L+Y I Y H+DF+ ++ A +VY
Sbjct: 327 VPIAVW--NGGKDLLADPQDVGLLLPKL---PNLIYHKEIPFYNHLDIFIWAMDAPQEVYN 381

Query: 396 DLIRFLREN 404
D++ + E+
Sbjct: 382 DIVSMISED 390

>gi|126307|sp|P04634|LIPG_RAT TRIACYLGLYCEROL LIPASE PRECURSOR (LIPASE, LINGUAL)
>gi|67160|pir||LIRTT triacylglycerol lipase (EC 3.1.1.3)
precursor, lingual - rat >gi|56596|emb|CAA26179|
(X02309) lipase precursor [Rattus norvegicus]
Length = 395

Score = 204 bits (514), Expect = 8e-52
Identities = 122/366 (33%), Positives = 194/366 (52%), Gaps = 16/366 (4%)

Query: 49 QLLLPLGYPCTEHNVETKDGFLSLQHIPHGKNAAD-STGPPVFLQHGLFQGGDTWFIN 107
Q++ GYPC E+ V T+DG++L + IPHGKN + + P V+LQHGL W N
Sbjct: 36 QMITYWGYPCEYEVVTEDEGYILGVYRIPHGKNNSENIGKRPVVYLQHGLIASATNWIAN 95

Query: 108 SAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFDWDSWQELAEYDLLAMLGY 167
SL ++LAD G+DVW+GN RG WS+ + +S FW +S+ E+A+YDL A + +
Sbjct: 96 LPNNSLAFMLADAGYDVWLGNSRGNTWSRKNVYSPDSVEFWAFSDEMAYDLPATINF 155

Query: 168 VYTVT-QSKILYVGHSQGTIMGLAAL-TMPEIVKMISSAALLCPISYLDHVSASF-VLRA 224
+ T Q KI YVGHSQGT +G A T P + K I + L P++ + + + +
Sbjct: 156 IVQKTGQEKIHYVGHSQGTITIGFIAFSTNPTLAKKIKTFYALAPVATVKYTQSPLKKISF 215

Query: 225 VAMHLDQMLV--TMGIHQNLFRSDMGVQIVDSLCDGEHVD--CNNLLSAITG-ENCCFNT 279
+ L +++ M + F +G ++ C E +D C+N L G + N
Sbjct: 216 IPTFLFKLMFGKKMFLPHTYFDDFLGTEV---CSREVLDLLCSNTLFIFCGFDKKNLNV 271

Query: 280 SRIDYYLEYEPHPSSTKNLHHLFQMIRKGTFAKYDYGLLG-NLRRYGHRLPPAFDLSSIP 338
SR D YL + P +S ++ H Q++R G F +++G N+ Y PP +D+S++
Sbjct: 272 SRFDVYLGHNPAGTSVQDFLHWAQLVRSGKFQAFNWGSPSQNMLHYNQKTPPEYDVSAMT 331

Query: 339 ESLPIWMGYGGLDALADVTDVQRTIRELGSTPELLYIGDYGHIDFVMSVKAKDDVYVDLI 398
+ +W GG D LAD DV + +L + I Y H+DF+ ++ A +VY ++I
Sbjct: 332 VPVAW--NGGNDILADPQDVAMLLPKLSNLLFHKEILAYNHLDFIAMDAPQEVYNEMI 389

Query: 399 RFLREN 404
+ E+
Sbjct: 390 SMMAED 395

>gi|2384863 (AF022976) Similar to lipase; R11G11.14 [Caenorhabditis elegans]
Length = 405

Score = 199 bits (500), Expect = 4e-50
Identities = 118/366 (32%), Positives = 183/366 (49%), Gaps = 18/366 (4%)

Query: 49 QLLLPLGYPCTEHNVETKDGFLSLQHIPHGKNAADSTG--PPVFLQHGLFQGGDTWFI 106
Q++ GYP ++V T DG++L L IPHGK G P VF+QHGL W +
Sbjct: 32 QIIERWGYPAMIYSVTDDGYILELHRIIPHGKTNVTPNGKQPVVFMQHGLLCASDWTM 91

Query: 107 NSAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFDWDSWQELAEYDLLAMLG 166
N EQS +I AD GFDVW+GN+RG +S H FW+WSW E+A YDL AM+
Sbjct: 92 NLPEQSAAFIFADAGFDVWLGNMGRNTYSMKHKNLKASHSDFWEWSWDEMATYDLPAMID 151

Query: 167 VYTVT-QSKILYVGHSQGTIMGLAALTMPE--IVKMISSAALLCPISYLDHVS--SFV 221
V VT Q + Y+GHSQGT+ + L+ + K I L P+ + + SF
Sbjct: 152 KVLEVTGQESLYYMGHSQGTITMFHLSKDDGIFAKKIKKFALAPVGSVKDIKFLSFF 211

Query: 222 LRAVAMHLDQMLVTMGIHQNLFRSDMGVQIVDSLCDGEHVD---CNNLLSAITG-ENCCF 277
++ D G + + +C G ++ C+N+ I G E+ +
Sbjct: 212 AHYFSLEFDGWFDFVGAGEFLPNNWAMKLAADICGGLKIESDLCDNVCFIAGPESDQW 271

Query: 278 NTSRIDYYLEYEPHPSSTKNLHHLFQMIRKGTFAKYDYGLLGNLRRYG-HLRPPAFDLSS 336
N++R+ Y ++P ++T+N+ H QM+R G YD+G N + PP +D ++
Sbjct: 272 NSTRVPVYASHDPAGTATQNIHVHIQMRHGGVPAYDWGSKENKKNVNFQANPPEYDFTA 331

Query: 337 IPESLPIWMGYGGLDALADVTDVQRTIRELGSTPELL----YIGDYGHIDFVMSVKAKDD 392
I + I++ + D LAD TD+ + P ++ Y DY H DFV ++A +D

Sbjct: 332 I-KGTQIYLYWSDADWLADKTDITNYLL-TRLNPAIIAQNNYFTDYNHFDVFVGLRAPND 389

Query: 393 VYVDLI 398

+Y+ ++

Sbjct: 390 IYLPV 395

>gi|3041702|sp|P80035|LIPG_CANFA TRIACYLGLYCEROL LIPASE PRECURSOR (LIPASE, GASTRIC)
>gi|2204113|emb|CAA74198| (Y13899) triacylglycerol
lipase [Canis familiaris]
Length = 398

Score = 198 bits (499), Expect = 5e-50

Identities = 123/364 (33%), Positives = 190/364 (51%), Gaps = 18/364 (4%)

Query: 49 QLLLPLGYPCTEHNVEKDGFLSLQHIPHG-KNKAADSTGPPVFLQHGLFQGGDTWFIN 107

Q++ GYP E+ V T+DG++L + IP+G KN P FLQHGL W N

Sbjct: 37 QMITYWGYPAEEYEVVTEGDYILGIDRIPYGRKNSENIGRRPVAFQLQHGLLASATNWISN 96

Query: 108 SAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFDWDSWQELAEYDLLAMLY 167

SL +ILAD G+DVW+GN RG W++ + +S FW +S+ E+A+YDL A + +

Sbjct: 97 LPNNSLAFILADAGYDVWLGNSRGNTWARRNLYYSPDSVEFWAFSDEMAYDLPATIDF 156

Query: 168 VYTVT-QSKILYVGHSGQTIMGLAAL-TMPEIVKMISSAALLCPISYLDHVSASF-VLRA 224

+ T Q K+ YVGHSGQT +G A T P++ K I + L P++ + + L

Sbjct: 157 ILKKTGQDKLHYVGHSGQTTIGFIAFSTNPKLAKRIKTFYALAPVATVKYTETLLNKLML 216

Query: 225 VAMHLDQMLVMTGIHQNLFRSDMGVQIVDSLCDGEHVD--CNNLLSAITG-ENCCFNSTR 281

V L +++ I + D + +C E VD C+N L I G + N SR

Sbjct: 217 VPSFLFKLIFGNKIFYPHFFDQ--FLATEVCSRETVDLLCSNALFIICGFTMNLMNSR 274

Query: 282 IDYYLEYEPHPSSTKNLHHLFQMIKGTFAKYDYGL-LGNLRRYGHRLPPAFDLSSIPES 340

+D YL + P +S +N+ H Q ++ G F +D+G + N+ Y PP ++L+ +

Sbjct: 275 LDVYLSHNPAQTSVQNVLHWSQAVKSGKFQAFDWGSPVQNMHMHQSMPPYNYLDMHVP 334

Query: 341 LPIWMGYGGLDALADVDVQRTIRELGSTPELly---IGDYGHIDFVMSVKAKDDVYVDL 397

+ +W GG D LAD DV + +L P L+Y I Y H+DF+ ++ A VY ++

Sbjct: 335 IAVW--NGGNDLLADPHDVLKLLSKL---PNLIYHRKIPPNHLDFIWAMDAPQAVYNEI 389

Query: 398 IRFL 401

+ +

Sbjct: 390 VSMM 393

>gi|505053 (U08464) lysosomal acid lipase [Homo sapiens]

>gi|506431|emb|CAA83495| (Z31690) lysosomal acid lipase

[Homo sapiens]

Length = 399

Score = 195 bits (490), Expect = 5e-49

Identities = 124/357 (34%), Positives = 185/357 (51%), Gaps = 12/357 (3%)

Query: 55 GYPCTEHNVEKDGFLSLQHIPHG-KNKAADSTGPPVFLQHGLFQGGDTWFINSAEQSL 113

G+P E+ VET+DG++L L IPHG KN + P VFLQHGL W N A SL

Sbjct: 45 GFPSEEYLVETEDGYILCLNRIPHGRKNHSDKGPKPVVFLQHGLLADSSNWVTNLANSLS 104

Query: 114 GYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFDWDSWQELAEYDLLAMLYVYTVT- 172

G+ILAD GFDVW+GN RG WS+ H T SV FW +S+ E+A+YDL A + ++ T

Sbjct: 105 GFILADAGFDVWGMNSRGNTWSRKHKTLVSQDEFWAFSYDEMAKYDLPASINFILNKTG 164

Query: 173 QSKILYVGHSGQTIMGLAALT-MPEIVKMISSAALLCPISYLDHVSASFV-LRAVAMHLD 230

Q ++ YVGHSGQT +G A + +PE+ K I L P++ + ++ L + HL

Sbjct: 165 QEQVYVGHSGQTTIGFIAFSQIPELAKRIKMFFALGPVASVAFCTSPMAKLGRLPDHLI 224

Query: 231 QMLV--TMGIHQNLFRSDMGVQIVDSLCDGEHVDCCNNLLSAITGEN-CCFNSTRIDYYLE 287

+ L + Q F +G + + E C NL + G N N SR+D Y

Sbjct: 225 KDLFGDKFLPQSAFLKWLGVCTHVLKEL--CGNLCFLCGFNERNLMSRVDVYTT 282

Query: 288 YEPHPSSTKNLHHLFQMIKGTFAKYDYGLLG-NLRRYGHRLPPAFDLSSIPESLPIWVG 346

+ P +S +N+ H Q ++ F +D+G N Y PP +++ + +W

Sbjct: 283 HSPAGTSVQNMHLWSQAVKFQKFAFDWGSASKNYFHYNQSYPPYTNVKDMLVPTAVWS- 341

Query: 347 YGGLDALADVTDVQRTIRELGSTPELLYIGDYGHIDFVMSVKAKDDVYVDLIRFLRE 403
GG D LADV DV + ++ + I ++ H+DF+ + A +Y +I +R+
Sbjct: 342 -GGHDWLADVVDVNILLTQITNLVHFESIPEWEHLDFIWGLDAPWRLYNKIINLMRK 397

>gi|585405|sp|P38571|LIPA_HUMAN LYSOSOMAL ACID LIPASE/CHOLESTERYL ESTER HYDROLASE PRECURSOR
(LAL)

(ACID CHOLESTERYL ESTER HYDROLASE) (STEROL ESTERASE)
(LIPASE A) (CHOLESTERYL ESTERASE) >gi|187152 (M74775)
lysosomal acid lipase/cholesterol esterase [Homo
sapiens]
Length = 399

Score = 195 bits (490), Expect = 5e-49
Identities = 124/357 (34%), Positives = 185/357 (51%), Gaps = 12/357 (3%)

Query: 55 GYPCTEHNVEVKDGFLLSLQHIPHG-KNKAADSTGPPVFLQHGFLFQGGDTWFINSAEQSL 113
G+P E+ VET+DG++L L IPHG KN + P VFLQHGGL W N A SL
Sbjct: 45 GFPSEELYVETEDGYILCLNRIPHGRKNHSDKGPKPVFLQHGGLADSSNWNLANSSL 104

Query: 114 GYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFDWDSWQELAEYDLLAMLGYYVYTVT- 172
G+ILAD GFDVW+GN RG WS+ H T SV FW +S+ E+A+YDL A + ++ T
Sbjct: 105 GFILADAGFDVWGMNSRUX:rm: ERROR: Cannot access blast2/.seq.eshpc01.1450600: No such
file or directory
GNTWSRKHKTLSVSQDEFWAFSYDEMAKYDLPASINFILNKTG 164

Query: 173 QSKILYVGHSQGTIMGLAALT-MPEIVKMISSAALLCPISYLDHVSASFV-LRAVAMHLD 230
Q ++ YVGHSQGT +G A + +PE+ K I L P++ + ++ L + HL
Sbjct: 165 QEQVYVVGHSQGTITIGFIAFSQIPELAKRIKMFFALGPVASVAFCTSPMAKLGRLPDHLI 224

Query: 231 QMLV--TMGIHQLNFRSDMGVQIVDSLCDGEHVDCNNLLSAITGEN-CCFNSTRIDYYLE 287
+ L + Q F +G + + E C NL + G N N SR+D Y
Sbjct: 225 KDLFGDKFLPQSAFLKWLGVTHVILKEL--CGNLCFLLCGFNERNLNM SRVDVYTT 282

Query: 288 YEPHPSSTKNLHHLFQMIRKGTFAKYDYGLLG-NLRRYGHRLRPPAFDLSSIPESLPIWMG 346
+ P +S +N+ H Q ++ F +D+G N Y PP +++ + +W
Sbjct: 283 HSPAGTSVQNMLHWSQAVKFQKFQAFDWGSSAKNYFHYNQSYPTYNVKDMLVPTAVWS- 341

Query: 347 YGGLDALADVTDVQRTIRELGSTPELLYIGDYGHIDFVMSVKAKDDVYVDLIRFLRE 403
GG D LADV DV + ++ + I ++ H+DF+ + A +Y +I +R+
Sbjct: 342 -GGHDWLADVVDVNILLTQITNLVHFESIPEWEHLDFIWGLDAPWRLYNKIINLMRK 397